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Project Title: Development of Markers Linked to FHB Resistance in Durum Wheat.

PROJECT 2 ABSTRACT

(1 Page Limit)

North Dakota leads the nation, by far, in total acreage and production of durum wheat. The extensive economic damage caused by *Fusarium* head blight (FHB) or scab to the North Dakota durum and wheat producers is well recognized. The most cost-effective way of reducing losses from this devastating disease is through the development of genetic resistance in the host plant. Once resistance genes are identified, transfer into adapted wheat germplasm remains a lengthy and difficult task because undesirable traits generally accompany the transfer. In durum wheat this process is confounded by the effect of hexaploid to tetraploid crosses and complications that arise due to the aneuploidy of an entire genome (D-genome). Additionally, certain regions prove to be less effective in durum background than bread wheat genetic background. Markers linked to resistance genes can accelerate selection, germplasm development and time to variety release expediting this process and providing diverse germplasm for durum breeding. In this project we will use existing markers in addition to markers currently being developed by a number of groups as a result of the ever increasing EST and sequence database to identify and develop "breeder friendly" markers to improve germplasm development and reduce time to variety release. The specific objectives of this project are to:

- 1) **identify QTL region(s) for FHB resistance in Wangshuibai derived RIL populations of durum wheat;**
- 2) **develop a PCR-based marker system for screening large durum breeding populations segregating for FHB; and**
- 3) **demonstrate the utility of these markers in populations developed for breeding programs.**

We have developed 274 Wangshuibai derived (from crosses to durum line D87130) recombinant inbred lines and are in the process of screening this population for molecular markers. Results from the two disease screening greenhouse seasons showed excellent correlations and indicated a great potential for use of these lines in developing resistant durum cultivars. In this proposal we plan to complete the QTL analysis of this population, verify the results by analyzing a set of backcross derived lines and identify PCR based markers linked to the resistance QTL(s). Markers may represent the only mean by which the resistance QTL from *T. dicoccoides*, Sumai3, Wangshuibai and other possible sources of resistance can eventually be combined in a single variety, the ultimate objective of this project